IMPACTS OF COST-EFFECTIVE HIGH-THROUGHPUT GENOTYPING OF LOBLOLLY PINE ON APPLIED TREE BREEDING PROGRAMS

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Advances in DNA sequencing technology over the past several years have increased the yield of DNA sequence per dollar by several orders of magnitude. Over the same time period, strategies have been developed for combining multiple DNA samples together to minimize labor costs and maximize the transfer of effort from researchers to computers. The combined result is that it is now possible to discover and describe genetic variation at far higher resolution than ever before, at a cost comparable to that of establishing and maintaining field trials for progeny-testing candidate selections. Costs of establishing, maintaining, and measuring field trials are likely to increase in the future, as labor and operating costs increase with inflation, while the cost of genotyping is likely to continue decreasing for at least the next few years. This is likely to lead to a situation in which obtaining progeny phenotypes to use in estimation of parental breeding values will be much more expensive than high-density genotyping of the parent trees. This change in the cost structure of phenotyping versus genotyping will lead to a new and unfamiliar set of opportunities for tree breeders to apply molecular markers in applied breeding programs. Exploiting these new opportunities in the most effective and efficient way is likely to require changes in strategies for breeding, selecting, and field testing. This presentation will describe the methods for tissue collection, DNA isolation, and cost-effective genotyping, and present data regarding the suitability of the resulting markers for genetic analysis in breeding and testing populations of loblolly pine.